	Number: 09/643 579 Changed a file from non-ASCII to ASCII ENTERED
	Changed the margins in cases where the sequence text was "wrapped" down to the next line.
	Edited a format error in the Current Application Data section, specifically:
	Edited the Current Application Data section with the actual current number. The number inputt applicant was the prior application data; or other
	Added the mandatory heading and subheadings for "Current Application Data".
	Edited the "Number of Sequences" (ield. The applicant spelled out a number instead of using a
	Changed the spelling of a mandatory field (the headings or subheadings), specifically:
	Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited v
	Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
	Corrected subheading placement. All responses must be on the same line as each subheading applicant placed a response below the subheading, this was moved to its appropriate place.
	Inserted colons after headings/subheadings. Headings edited included:
	Deleted extra, invalid, headings used by an applicant, specifically:
	Deleted: non-ASCII "garbage" at the beginning/end of files; secretary initials/filename a page numbers throughout text; other invalid text, such as Extrançous nate.
	Inserted mandatory headings, specifically:
	Corrected an obvious error in the response, specifically:
	Edited identifiers where upper case is used but lower case is required, or vice versa.
	Согrected an error in the Number of Sequences field, specifically:
_	A "Pland Page Break" code was inserted by the applicant. All occurrences had to be deleted.
_	eleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field according to a Patentin bug). Sequences corrected:
t	

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. 00 NOT send a copy of this form.

4 -- '

OIPE

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Output Set: N:\CRF3\09142000\1643579.raw
                      SEQUENCE LISTING
      3 (1) GENERAL INFORMATION:
             (i) APPLICANT: RICHARD MARTIN BROGLIE
C-->
                             LORIN ROGER DE BONTE
                              WILLIAM DEAN HITZ
                              GUO-HUA MIAO
                             ROBERT STEFAN REITER
            (ii) TITLE OF INVENTION: GENES FOR MUTANT MICROSOMAL
                                       FATTY ACID DELTA-12
     12
                                       DESATURASES AND RELATED
     13
                                       ENZYMES FROM PLANTS
     14
           (iii) NUMBER OF SEQUENCES: 17
     16
            (iv) CORRESPONDENCE ADDRESS:
     18
                   (A) ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
     19
                   (B) STREET: 1007 MARKET STREET
     20
     21
                   (C) CITY: WILMINGTON
                   (D) STATE: DELAWARE
                   (E) COUNTRY: U.S.A.
                   (F) ZIP: 19898
             (V) COMPUTER READABLE FORM:
     26
                   (A) MEDIUM TYPE: FLOPPY DISK
                   (B) COMPUTER: IBM PC COMPATIBLE
     28
                   (C) OPERATING SYSTEM: MICROSOFT WINDOWS 95
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                   (D) SOFTWARE: MICROSOFT OFFICE 97
     30
            (vi) CURRENT APPLICATION DATA:
     32
                   (A) APPLICATION NUMBER: US/09/643,579
C--> 33
C--> 34
                   (B) FILING DATE: 22-Aug-2000
                   (C) CLASSIFICATION:
     35
           (vii) PRIOR APPLICATION DATA:
     37
                   (A) APPLICATION NUMBER: 08/256,047
     38
                   (B) FILING DATE: NOVEMBER 17, 1992
     39
          (viii) ATTORNEY/AGENT INFORMATION:
     41
                   (A) NAME: Lynne M. Christenbury
(C) REFERENCE/DOCKET NUMBER: BB-1334-A
     42
     43
             (ix) TELECOMMUNICATION INFORMATION:
     45
                   (A) TELEPHONE: (302) 992-5481
     46
     47
                   (B) TELEFAX: (302) 892-7949
                   (C) TELEX:
     51 (2) INFORMATION FOR SEQ ID NO: 1:
              (i) SEQUENCE CHARACTERISTICS:
                   (A) LENGTH: 1464 base pairs
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                   (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
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                   (D) TOPOLOGY: linear
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             (ii) MOLECULE TYPE: cDNA
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PATENT APPLICATION: US/09/643,579

See P.

DATE: 09/14/2000

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(ix) FEATURE:

(A) NAME/KEY: CDS

RAW SEQUENCE LISTING PATENT APPLICATION: US/09/643,579

DATE: 09/14/2000 TIME: 16:49:22

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Output Set: N:\CRF3\09142000\1643579.raw

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C> 65 (XI) SEQUENCE DESCRIPTION: SEQ ID NO: I: 67 GGCACGAGCT CGTGCCGAAT TCGGCACGAG AGGAGACAGA GAGAGAGATT GAGGAGGAC 69 TTCTTCGTAG GGTTCATCGT TATTAACGTT AAATCTTCAT CCCCCCCTAC GTCAGCCAGC 71 TCAAGAAAC ATG GGT GCA GGT GGA AGA ATG CAA GTG TCT CCT CCC TCC 72 Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser 73 1 5 10 75 AAA AAG TCT GAA ACC GAC AAC ATC AAG CGC GTA CCC TGC GAG ACA CCG 76 Lys Lys Ser Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro 77 15 20 25 79 CCC TTC ACT GTC GGA GAA CTC AAG AAA GCA ATC CCA CCG CAC TGT TTC 79 CCC TTC ACT GTC GGA GAA CTC AAG AAA GCA ATC CCA CCG CAC TGT TTC 80 Pro Phe Thr Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe 81 30 45 83 AAA CGC TCG ATC CCT CGC TCT TTC TCC TAC CTC ATC TGG GAC ATC ATC 84 Lys Arg Ser Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile 85 50 87 ATA GCC TCC TGC TTC TAC TAC GTC GCC ACC ACT TAC TGC GAC ATC CTC 88 Ile Ala Ser Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu 89 65 91 CCT CAC GCT CTC TCC TAC TGC GCC ACC ACT TAC TGC GCC TGC CTC 88 Ile Ala Ser Cys Phe Tyr Tyr Val Ala Trp Pro Leu Tyr Trp Ala Cys Gln 92 Pro His Pro Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln 93 80 95 GGC TGC GTC CTA ACC GGC GTC TGG GTC ATA GCC CAC GAG TGC CAC 96 Gly Cys Val Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His 100 97 98 CAC GCC TCC AGC GAC TAC CAG TGG GTC ATA GCC CAC GAG TGC CAC 100 His Ala Phe Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile 101 110 115 103 TTC CAC TCC TCC CTC CTC CTC TAC TTC TCC TGG AAG TAC AGT CAT 104 Phe His Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His 105 130 107 CGA CGC CAC CAT TCC AAC ACC GGC TCC CTC TAC TGC GAAG TAC AGT CAT 108 Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe 109 145 111 GTC CCC AAG AAG AAG AAC ACC ACC GTG GAC AAC GAA CTC TAC 112 TCC CCC AAG AAG AAG AAC ACC ACC TC TAC TAC 113 TCC CCC AAG AAG AAG AAC ACC ACC ACT TCC TCC AAC 113 TCC CCC AAG AAG AAG AAC ACC ACC ACT TCC TCC AAC 114 TCC CCC AAG AAG AAC AAC ACC ACC TTC TTC TCC TC AAC 115 TCC CCC AAG AAG AAC AAC ACC ACC TTC TTC TCC TCC TCC
67 GGCACGAGCT CGTGCCGAAT TCGGCACCAGA AGGAGACACAAC AGGAGAGACACAC 68 TTCTTCGTAG GGTTCATCGT TATTAACGTT AAATCTTCAT CCCCCCCTAC GTCAGCCCAGC 120 TTCAAGAAAC ATG GGT GCA GGT GGA AGA ATG CAA GTG TCT CCT CCC TCC 168 TCAAGAAAC ATG GGT GCA AGGA AGA ATG CAA GTG TCT CCT CCC TCC 168 TCAAGAAAC ATG GGT GGA AGA AGA AGA AGA AGA AGA AGA
69 TTCTTCGTAG GGTTCATCGT TATTACGTT AAACT AAG CTA ATC CTC CCC TCC 71 TCAAGAAAC ATG GGT GGA AGG AGG AGG AGG AGG ATG CTT CCT CCC TCC 72
TCAAGAAAC ATG GGT GCA GGT GGA AGA RIC CAA GT CAC TO TO Pro Ser
72
73
75 AAA AAG TCT GAA ACC GAC AAC ATC AAG CGC GTA CCC TGC GAG ACA CCG 76 Lys Lys Ser Glu Thr Asp Asn 11e Lys Arg Val Pro Cys Glu Thr Pro 77 15 20 25 79 CCC TTC ACT GTC GGA GAA CTC AAG AAA GCA ATC CCA CCG CAC TGT TTC 80 Pro Phe Thr Val Gly Glu Leu Lys Lys Ala 11e Pro Pro His Cys Phe 81 30 83 AAA CGC TCG ATC CCT CGC TCT TTC TCC TAC CTC ATC TGG GAC ATC ATC 84 Lys Arg Ser 11e Pro Arg Ser Phe Ser Tyr Leu 11e Trp Asp 11e 11e 85 87 ATA GCC TCC TGC TTC TAC GTC GCC ACC ACT TAC TTC CCT CTC 88 11e Ala Ser Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu 89 65 91 CCT CAC GCT CTC TCC TAC TTC GCC ACC ACT TAC TGG GCC TGC CAG 92 Pro His Pro Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln 93 80 95 GGC TGC GTC CTA ACC GGC GTC TGG GTC ATA GCC CAC GAG TGC GGC CAC 96 Gly Cys Val Leu Thr Gly Val Trp Val 11e Ala His Glu Cys Gly His 97 95 GAC GCC TTC AGC GAC TAC CAG TGG CTG GAC ACC GTC GGC CTC ATC 100 His Ala Phe Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu 11e 101 110 115 120 120 125 126 445 456 464 475 476 477 477 478 479 479 479 479 470 470 470 470 470 470 470 470 470 470
76 Lys Lys Ser Glu Thr Asp Ash 11e Lys Alg 25 77 15 20 20 79 CCC TTC ACT GTC GGA GAA CTC AAG AAA GCA ATC CCA CCG CAC TGT TTC 80 Pro Phe Thr Val Gly Glu Leu Lys Lys Ala 11e Pro Pro His Cys Phe 81 30 83 AAA CGC TCG ATC CCT CGC TCT TTC TCC TAC CTC ATC TGG GAC ATC ATC 84 Lys Arg Ser 11e Pro Arg Ser Phe Ser Tyr Leu 11e Trp Asp 11e 11e 85 50 87 ATA GCC TCC TGC TTC TAC TAC GTC GCC ACC ACT TAC TTC CCT CTC 88 I1e Ala Ser Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu 89 65 91 CCT CAC CTC TCC TAC TTC GCC TGG CCT CTC TAC TGG GCC TGC CAG 92 Pro His Pro Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln 93 95 GGC TGC GTC CTA ACC GGC GTC TGG GTC ATA GCC CAC GAG TGC GGC CAC 96 Gly Cys Val Leu Thr Gly Val Trp Val 11e Ala His Glu Cys Gly His 97 95 90 CAC GCC TTC AGC GAC TAC CAG TGG CTG GAC ACC GTC GGC CTC ATC 100 His Ala Phe Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu I1e 101 110 115 120 125 107 108 Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe 109 145 111 GTC CCC AAG AAG AAG TCA AAC TAC AAG TGG TAC GAC AAC GAC AAC GAC AAC GAA GAA CAC 112 CCC AAG AAG AAG TCA AAC TAC AAG TGG TAC GAC AAC TAC CAC AAC TAC TTC TCC TAC TTC TT
77
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81 30
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87 ATA GCC TCC TGC TTC TAC TAC GTC GCC ACC ACT TAC TTC CCT CTC CTC 88 Ile Ala Ser Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu 89 65 70 75 91 CCT CAC GCT CTC TCC TAC TTC GCC TGG CCT CTC TAC TGG GCC TGC CAG 92 Pro His Pro Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln 93 80 85 95 GGC TGC GTC CTA ACC GGC GTC TGG GTC ATA GCC CAC GAG TGC GGC CAC 96 Gly Cys Val Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His 97 95 100 105 99 CAC GCC TTC AGC GAC TAC CAG TGG CTG GAC ACC GTC GGC CTC ATC 100 His Ala Phe Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile 101 110 115 120 125 103 TTC CAC TCC TTC CTC CTC GTC CCT TAC TTC TCC TGG AAG TAC AGT CAT 104 Phe His Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His 105 130 135 107 CGA CGC CAC CAT TCC AAC ACT GGC TCC CTC GAG AGA GAC GAC GAC GAC GAC GAC GAC GA
88 Ile Ala Ser Cys Phe Tyr Tyr Val Ala Int
89 65 91 CCT CAC GCT CTC TAC TTC GCC TGG CCT CTC TAC TGG GCC TGC CAG 92 Pro His Pro Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln 93 80 85 95 GGC TGC GTC CTA ACC GGC GTC TGG GTC ATA GCC CAC GAG TGC GGC CAC 96 Gly Cys Val Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His 97 95 99 CAC GCC TTC AGC GAC TAC CAG TGG CTG GAC GAC ACC GTC GGC CTC ATC 100 His Ala Phe Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile 101 110 115 120 125 103 TTC CAC TCC TTC CTC CTC GTC CCT TAC TCC TGG AAG TAC AGT CAT 104 Phe His Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His 105 130 135 107 CGA CGC CAC CAT TCC AAC ACT GGC TCC CTC GAG AGA GAC GAA GTG TTT 108 Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe 109 145 150 111 GTC CCC AAG AAG AAG AAG ACA GAC ACT GAG TAC GGC AAG TAC CTC AAC 112 Val Pro Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn
91 CCT CAC CCT CTC TAC TAC TTC GCC TGG CCT CTC TAC TGG GCC TGC CAG 92 Pro His Pro Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln 93 80 85 90 95 GGC TGC GTC CTA ACC GGC GTC TGG GTC ATA GCC CAC GAG TGC GGC CAC 96 Gly Cys Val Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His 97 95 100 105 99 CAC GCC TTC AGC GAC TAC CAG TGG CTG GAC GAC ACC GTC GGC CTC ATC 100 His Ala Phe Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile 101 110 115 120 125 103 TTC CAC TCC TTC CTC CTC GTC CCT TAC TTC TCC TGG AAG TAC AGT CAT 104 Phe His Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His 105 130 135 107 CGA CGC CAC CAT TCC AAC ACT GGC TCC CTC GAG AGA GAC GAA GTG TTT 108 Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe 109 145 150 111 GTC CCC AAG AAG AAG ACA GAC ACT GAC TTC TYR Tyr Gly Lys Tyr Leu Asn 112 Val Pro Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn
92 Pro His Pro Leu Ser Tyr Phe Ala Trp Plo Deu 197 90 80 85 90 85 90 90 85 90 85 90 90 85 90 85 90 90 85 90 90 85 90 90 90 90 90 90 90 90 90 90 90 90 90
93 80 85 95 GGC TGC GTC CTA ACC GGC GTC TGG GTC ATA GCC CAC GAG TGC GGC CAC 96 Gly Cys Val Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His 97 95 100 105 99 CAC GCC TTC AGC GAC TAC CAG TGG CTG GAC GAC ACC GTC GGC CTC ATC 100 His Ala Phe Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile 101 110 115 120 125 103 TTC CAC TCC TTC CTC CTC GTC CCT TAC TCC TGG AAG TAC AGT CAT 104 Phe His Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His 105 130 135 107 CGA CGC CAC CAT TCC AAC ACT GGC TCC CTC GAG AGA GAC GAA GTG TTT 108 Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe 109 145 150 111 GTC CCC AAG AAG AAG ACA GAC ACT AAC TGG TAC GGC AAG TAC CTC AAC 112 Val Pro Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn
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96 Gly Cys Val Leu Thr Gly Val Trp Val Tle Ara Tile Ara T
97 95 100 99 CAC GCC TTC AGC GAC TAC CAG TGG CTG GAC ACC GTC GGC CTC ATC 100 His Ala Phe Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile 110 110 125 103 TTC CAC TCC TTC CTC CTC GTC CCT TAC TTC TCC TGG AAG TAC AGT CAT 104 Phe His Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His 105 130 135 140 107 CGA CGC CAC CAT TCC AAC ACT GGC TCC CTC GAG AGA GAC GAA GTG TTT 108 Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe 109 145 150 111 GTC CCC AAG AAG AAG AAG TCA GAC ATC AAG TGG TAC GGC AAG TAC CTC AAC 112 Val Bro Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn
97 95 99 CAC GCC TTC AGC GAC TAC CAG TGG CTG GAC ACC GTC GGC CTC ATC 100 His Ala Phe Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile 115 120 125 101 110 125 103 TTC CAC TCC TTC CTC CTC GTC CCT TAC TCC TGG AAG TAC AGT CAT 104 Phe His Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His 105 130 135 107 CGA CGC CAC CAT TCC AAC ACT GGC TCC CTC GAG AGA GAC GAA GTG TTT 108 Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe 109 145 150 111 GTC CCC AAG AAG AAG AAG ACA GAC AAC ACT GGC TAC GGC TAC GGC AAG TAC CTC AAC 112 Val Pro Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn
100 His Ala Phe Ser Asp Tyr GIn Trp Lett Asp Asp Tin Value 125 101 110 115 115 120 120 125 103 TTC CAC TCC TTC CTC GTC CCT TAC TTC TCC TGG AAG TAC AGT CAT 104 Phe His Ser Phe Lett Lett Val Pro Tyr Phe Ser Trp Lys Tyr Ser His 105 130 135 140 107 CGA CGC CAC CAT TCC AAC ACT GGC TCC CTC GAG AGA GAC GAA GTG TTT 108 Arg Arg His His Ser Asn Thr Gly Ser Lett Glu Arg Asp Glu Val Phe 109 145 110 GTC CCC AAG AAG AAG AAG AAC AAC AAC AAC TGG TAC GGC AAG TAC CTC AAC 111 GTC CCC AAG AAG AAG AAG TCA GAC AAC TGG TAC GGC AAG TAC CTC AAC 112 Val Pro Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Lett Asn
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112 Val P10 Lys Lys Lys Les 165
113 160 175 AAC CCT TTG GGA CGC ACC GTG ATG TTA ACG GTT CAG TTC ACT CTC GGC 69
116 Asn Pro Leu Gly Arg Thr Val Met Leu Till Val Gin The 1112 202 202
117 175 119 TGG CCT TTG TAC TTA GCC TTC AAC GTC TCG GGG AGA CCT TAC GAC GGC 74
120 Trp Pro Leu Tyr Leu Ala Phe Ash Val Sel Gly Alg 110 172 172 205
THE TAC AND MICE CAN COL AAC GCT CCC ATC TAC AAC GAC COL
124 Gly Phe Ala Cys His Phe His Pro Ash Ala Pio IIc 212
124 Gly Phe Ala Cys His Phe His Pro Asii Ala F10 112 17 220
124 Gly Phe Ala Cys His Phe His Pro Asia Ala File 1220 125 210 215 220 84
124 Gly Phe Ala Cys His Phe His Pro Ash Ala Pro 1220

RAW SEQUENCE LISTING DATE: 09/14/2000 PATENT APPLICATION: US/09/643,579 TIME: 16:49:22

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   139 ATC ACT TAC TTG CAG CAC ACG CAT CCT TCC CTG CCT CAC TAT GAC TCG
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    140 Ile Thr Tyr Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser
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    144 Ser Glu Trp Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp 145 290 295 300
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    148 Tyr Gly Ile Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val
149 305 310 315
    151 GCG CAT CAC CTG TTC TCG ACC ATG CCG CAT TAT CAT GCG ATG GAA GCT 152 Ala His His Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala
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    159 ACG CCG GTG GTT AAG GCG ATG TGG AGG GAG GCG AAG GAG TGT ATC TAT
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    160 Thr Pro Val Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr
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    163 GTG GAA CCG GAC AGG CAA GGT GAG AAG AAA GGT GTG TTC TGG TAC AAC
                                                                                 1272
    164 Val Glu Pro Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn 370 370 380
    167 AAT AAG TTA TGAAGCAAAG AAGAAACTGA ACCTTTCTCT TCTATGATTG
                                                                                  1321
     170 TCTTTGTTTA AGAAGCTATG TTTCTGTTTC AATAATCTTA ATTATCCATT TTGTTGTGTT
     1441
                                                                                  1464
     174 ΑΑΑΑΑΑΑΑΑΑ ΑΑΑΑΑΑΑΑΑΑ ΑΑΑ
     176 (2) INFORMATION FOR SEQ ID NO: 2:
              (i) SEQUENCE CHARACTERISTICS:
     178
                   (A) LENGTH: 384 amino acids
     179
                    (B) TYPE: amino acid
(D) TOPOLOGY: linear
     181
             (ii) MOLECULE TYPE: protein
     183
             (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
C--> 185
     187 Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser 188 1
     190 Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
191 20 25 30
     193 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
194 35 40
     196 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser
197 50 55 60
     199 Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
```

RAW SEQUENCE LISTING DATE: 09/14/2000 PATENT APPLICATION: US/09/643,579 TIME: 16:49:22 Input Set : A:\Cpg.pto Output Set: N:\CRF3\09142000\I643579.raw 202 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val 85 205 Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe 206 100 105 110 208 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser 209 115 120 125 211 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His 212 130 135 140 212 214 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys 215 145 150 160 217 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu 218 165 170 175 220 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu 221 180 185 190 223 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala 224 195 200 205 226 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu 227 210 215 220 229 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu 230 225 230 235 240 232 Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr 233 245 250 255 235 Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr 236 265 270 238 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp 239 275 280 285

241 Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
242 290 295 300

244 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
245 305
247 Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
248 325

250 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
251 340 345 355

253 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
254 355

256 Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu 257 370 375 380 259 (2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1155 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA

269 (iii) HYPOTHETICAL: NO
271 (iv) ANTI-SENSE: NO
273 (vi) ORIGINAL SOURCE:

261

262

263

264

265

W--> 267

(A) ORGANISM: Brassica napus

RAW SEQUENCE LISTING DATE: 09/14/2000 PATENT APPLICATION: US/09/643,579 TIME: 16:49:22

Input Set : A:\Cpg.pto

Output Set: N:\CRF3\09142000\1643579.raw

```
(vii) IMMEDIATE SOURCE
                     (B) CLONE: IMC129
              (ix) FEATURE:
                     (D) OTHER INFORMATION: G to A transversion
     281 mutation at nucleotide 316
     282 of the D form
              (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
C--> 284
     286 ATG GGT GCA GGT GGA AGA ATG CAA GTG TCT CCT CCC TCC AAA AAG TCT
     287 Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser
                                                  10
     288
     290 GAA ACC GAC AAC ATC AAG CGC GTA CCC TGC GAG ACA CCG CCC TTC ACT
     291 Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr 292 20 25 30
     294 GTC GGA GAA CTC AAG AAA GCA ATC CCA CCG CAC TGT TTC AAA CGC TCG
     295 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
                                      40
     298 ATC CCT CGC TCT TTC TCC TAC CTC ATC TGG GAC ATC ATC ATA GCC TCC
                                                                                       192
     299 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser
     302 TGC TTC TAC TAC GTC GCC ACC ACT TAC TTC CCT CTC CTC CCT CAC CCT
                                                                                       240
     303 Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
                                 70
     306 CTC TCC TAC TTC GCC TGG CCT CTC TAC TGG GCC TGC CAG GGC TGC GTC
                                                                                       288
     307 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
308 85 . ,90 95
     310 CTA ACC GGC GTC TGG GTC ATA GCC CAC AAG TGC GGC CAC CAC GCC TTC
                                                                                       336
     311 Leu Thr Gly Val Trp Val Ile Ala His Lys Cys Gly His His Ala Phe 312 100 105 110
     314 AGC GAC TAC CAG TGG CTG GAC GAC ACC GTC GGC CTC ATC TTC CAC TCC
                                                                                       384
     315 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser 316 115 120 125
     318 TTC CTC CTC GTC CCT TAC TTC TCC TGG AAG TAC AGT CAT CGA CGC CAC
                                                                                       432
     319 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
            130
                                    135
                                                           140
     322 CAT TCC AAC ACT GGC TCC CTC GAG AGA GAC GAA GTG TTT GTC CCC AAG
                                                                                       480
     323 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys 324 145 150 155 160
     324 145
     326 AAG AAG TCA GAC ATC AAG TGG TAC GGC AAG TAC CTC AAC AAC CCT TTG
                                                                                       528
     327 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu 328 165 170 175
     330 GGA CGC ACC GTG ATG TTA ACG GTT CAG TTC ACT CTC GGC TGG CCT TTG
331 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
332 180 185 190
                                                                                       576
     334 TAC TTA GCC TTC AAC GTC TCG GGG AGA CCT TAC GAC GGC GGC TTC GCT 335 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala
                                                                                      624
                                         200
                                                                205
                  195
     338 TGC CAT TTC CAC CCC AAC GCT CCC ATC TAC AAC GAC CGC GAG CGT CTC
     339 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
             210
                                    215
```

£41.

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

DATE: 09/14/2000 VERIFICATION SUMMARY TIME: 16:49:23 PATENT APPLICATION: US/09/643,579

Input Set : A:\Cpg.pto

Output Set: N:\CRF3\09142000\1643579.raw

```
L:5 M:220 C: Keyword misspelled or invalid format, [(i) APPLICANT:]
L:33 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:34 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:65 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:185 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:284 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:267 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3, Value=[DNA]
L:393 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:487 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:475 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5, Value=[DNA]
L:596 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:695 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:698 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7, Value=[DNA]
L:804 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:888 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:902 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:902 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:916 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:930 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:944 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:958 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:972 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ TD NO:]
L:986 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:1016 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1018 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
```

OIPE

```
RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/643,579

DATE: 09/06/2000
TIME: 11:53:03
```

Input Set : A:\BB1334A Corrected Seq Listing.txt
Output Set: N:\CRF3\09062000\I643579.raw

SEQUENCE LISTING

```
3 (1) GENERAL INFORMATION:
               (i) APPLICANT: RICHARD MARTIN BROGLIE
C-->
                               LORIN ROGER DE BONTE
      6
                                WILLIAM DEAN HITZ
                                GUO-HUA MIAO
      8
                                ROBERT STEFAN REITER
              (ii) TITLE OF INVENTION: GENES FOR MUTANT MICROSOMAL
       g
     11
                                          FATTY ACID DELTA-12
     12
                                          DESATURASES AND RELATED
     13
                                          ENZYMES FROM PLANTS
      14
             (iii) NUMBER OF SEQUENCES: 17
      16
              (iv) CORRESPONDENCE ADDRESS:
      18
                     (A) ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
      19
                     (B) STREET: 1007 MARKET STREET
      20
                     (C) CITY: WILMINGTON
(D) STATE: DELAWARE
      21
      22
                     (E) COUNTRY: U.S.A.
      23
                     (F) ZIP: 19898
      24
               (V) COMPUTER READABLE FORM:
      26
                     (A) MEDIUM TYPE: FLOPPY DISK
                     (B) COMPUTER: IBM PC COMPATIBLE
(C) OPERATING SYSTEM: MICROSOFT WINDOWS 95
(D) SOFTWARE: MICROSOFT OFFICE 97
      28
      29
      30
              (vi) CURRENT APPLICATION DATA:
      32
                     (A) APPLICATION NUMBER: US/09/643,579
      33
C-->
                     (B) FILING DATE: 22-Aug-2000
C-->
      34
                     (C) CLASSIFICATION:
      35
              (vii) PRIOR APPLICATION DATA:
      37
                      (A) APPLICATION NUMBER: 08/256,047
       38
                      (B) FILING DATE: NOVEMBER 17, 1992
       39
             (viii) ATTORNEY/AGENT INFORMATION:
                      (A) NAME: Lynne M. Christenbury
       42
                      (C) REFERENCE/DOCKET NUMBER: BB-1334-A
       43
               (ix) TELECOMMUNICATION INFORMATION:
       45
                     (A) TELEPHONE: (302) 992-5481
(B) TELEFAX: (302) 892-7949
       47
                      (C) TELEX:
       48
```

ERRORED SEQUENCES

```
990 (2) INFORMATION FOR SEQ ID NO: 17:
992 (i) SEQUENCE CHARACTERISTICS:
993 (A) LENGTH: 5 amino acids
994 (B) TYPE: amino acid
995 (C) STRANDEDNESS:
```

Does Not Comply
Corrected Diskette Needed
Error was edited

```
PATENT APPLICATION: US/09/643,579
                  Input Set : A:\BB1334A Corrected Seq Listing.txt
                  Output Set: N:\CRF3\09062000\1643579.raw
                 (D) TOPOLOGY: linear
    996
           (ii) MOLECULE TYPE: peptide
    998
           (iii) HYPOTHETICAL: YES.
    1000
            (iv) ANTI-SENSE: NO
    1002
             (v) FRAGMENT TYPE: internal
    1004
            (ix) FEATURE:
    1006
                  (A) NAME/KEY: Modified-site
    1007
                  (B) LOCATION: 2
    1008
                  (D) OTHER INFORMATION: /product= "Asp or Glu"
    1009
            (ix) FEATURE:
    1011
                  (A) NAME/KEY: Modified-site
    1012
                  (B) LOCATION: 4
    1013
                  (D) OTHER INFORMATION: /product= "Ala or Gly"
    1014
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:
C--> 1016
W--> 1018 His Xaa Cys Xaa His
    1019 1
E--> 1021 17
E--> 1023 XX-XXXX
           Extreneous material at end of file
E--> 1026 17
           needs to be deleted.
```

RAW SEQUENCE LISTING

DATE: 09/06/2000

TIME: 11:53:03

VERIFICATION SUMMARY

DATE: 09/06/2000 TIME: 11:53:04

PATENT APPLICATION: US/09/643,579 TIME: 11
Input Set : A:\BB1334A Corrected Seq Listing.txt

Output Set: N:\CRF3\09062000\1643579.raw

```
L:5 M:220 C: Keyword misspelled or invalid format, [(i) APPLICANT:]
L:33 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:34 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:65 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:185 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:284 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:267 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3, Value=[DNA]
L:393 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:487 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:475 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5, Value=[DNA]
L:4/5 M:240 W: Invalid value of Alpha Sequence header Fleid, [MODECORE 117E.], Sequence 15.596 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:] L:695 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:678 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7, Value=[DNA]
 L:804 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:888 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:902 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:916 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:916 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:930 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:944 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:958 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:958 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:986 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:906 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1016 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1018 M:341 W: (46) "n" or "Xaa" used. for SEO ID#:17
  L:1018 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1021 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
  L:1023 M:333 E: Wrong sequence grouping, Amino acids not in groups!
  L:1023 M:330 E: (2) Invalid Amino Acid Designator, 1
  M:332 Repeated in SeqNo=17
  L:1026 M:203 E: No. of Seq. differs, LENGTH:Input:5 Found:6 SEQ:17
```